

Relative efficiency = $\frac{\text{mean square error in RCBD design}}{\text{mean square error in triple lattice design}} \times 100$ (Gomez and Gomez (1984).

Genetic diversity was estimated from quantitative traits of genotypes using Euclidean distance (Unweighted Pair-group methods with Arithmetic Means (UPGMA)) computed by Statistical Software.

3. RESULTS AND DISCUSSION

3.1. Analysis of Variance

The analysis of variance showed highly significant differences ($P < 0.01$) among wheat genotypes for all studied traits (Table 3). Such considerable range of variations would provide a good opportunity for yield improvement. The results also justify carrying out further genetic analysis considering all (12) agro-morphology traits. The relative efficiency of triple lattice design was greater than one for more than half quantitative traits but it was greater than 0.95 for all quantitative traits indicating the advantage of triple lattice design over RCBD in increasing the experimental precision (Table 3). Masood *et al.* (2008) and Idrees and Khan, (2009) reported that alpha lattice designs were on the average more efficient in reducing the experimental error and hence provide the efficient estimation of treatment contrasts. Hence, the present analyses were done using triple-lattice design. Coefficients of variation in percent were also used to compare the precision of the experimentation, i.e., means with lower CV% for most of the characters revealed the reliability of the data collected from the experiment (Gomez and Gomez, 1984).

Adhiena *et al.* (2016) conducted genetic divergence study in 26 bread wheat genotypes considering twelve traits in Southern Zone of Tigray Regional State, at mid and highland areas. They reported the presence of significant differences among genotypes for all traits except for plant height and number of spikelets per plant. According to Dawit *et al.* (2012), days to maturity, number of tillers per plant, biological yield and harvest index were not significantly different in durum wheat genotypes. This disparity may be due to the differences in the genotypes and test environments used in different studies.

Table 3. Mean squares from analysis of variance for twelve traits of thirty-six bread wheat genotypes evaluated at Mehoni in 2017

Traits	Replications (d.f =2)	Block Within replication (Adj.) (df=15)	Treatments (d.f=35)		Intra block Error (d.f=55)	RCBD Error	Rel. to effic. (%)	CV (%)
			(Unadj)	(Adj)				
Plant height (cm)	1293.51**	20.43**	94.92	91.22**	17.49	18.12	100.51	4.88
Days to heading (days)	7.06**	4.82**	142.80	122.83**	4.04	4.21	100.64	2.80
Grain filling period (days)	2.26ns	5.71**	28.04	27.50**	6.12	6.08	98.39	8.59
Days to maturity (days)	1.69ns	9.04**	157.00	132.74**	8.13	8.32	100.24	2.84
No. of fertile tillers/plant (no.)	0.11ns	0.07ns	0.50	0.38**	0.09	0.08	95.67	13.53
Spike length (cm)	0.14ns	0.24ns	2.70	2.17**	0.25	0.25	98.89	5.28
No. of spikelets/spike (no.)	0.22ns	0.98ns	7.31	6.48**	1.21	1.16	95.92	5.98
No. of kernels/ spike(no.)	15.53**	17.32**	65.39	56.24**	12.22	13.31	102.49	7.54
1000-kernel weight (g)	3.77ns	12.70**	58.66	53.33**	12.99	12.93	99.51	10.07
Grain yield (t ha ⁻¹)	0.14ns	0.09ns	1.13	0.96**	0.12	0.12	94.46	8.38
Biomass yield (t ha ⁻¹)	0.04ns	0.08ns	0.25	0.25**	0.10	0.09	95.31	10.26
Harvest index (%)	2.09ns	7.83**	82.19	74.19**	6.91	7.11	100.33	7.60

Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively. DF= degree freedom
Rel.effic. = relative efficiency, RCBD= randomized completely randomized design, CV= coefficient of variations and adj. and uadj. =
adjusted or unadjusted treatment

3.2. Principal Component Analysis

Principal component analysis showed that the gross variability observed among the 36 test genotypes can be explained with four principal components with eigen values greater than unity (Table 4). The first four components together accounted for about 70.56% of the total variation among the genotypes with respect to all the 12 traits evaluated and showed the presence of considerable genetic diversity among the genotypes for most of the traits under consideration. Individually, PC1, PC2, PC3 and PC4 in that order accounted for about 33% 18%, 10% and 9% of the gross variation among the 36 bread wheat genotypes evaluated for 12 traits.

The traits, which contributed more to PC1, were days to maturity, days to heading, harvest index and number of spikelet per spike, whereas for second PC, grain yield, plant height, number of kernels per spike and spike length, for the third PC, biomass yield and number of fertile tillers per plant and for the fourth PC, grain filling period and 1000-kernel weight. The first two principal components PC1 and PC2 with values of 33% and 18% respectively, contributed more than half to the total variation. Therefore, the present study confirmed that the bread wheat genotypes showed significant variations for the characters studied and it suggested many opportunities for genetic improvement through selection. Similar works have been done by Khodadadi *et al.* (2011), Dawit *et al.* (2012) and Ashraf *et al.* (2012) and Awale and Sentayehu (2013) for grouping of genotypes by principal component analysis. Singh *et al.* (2014) also reported that the character contributing the maximum to divergence should be given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization.

Table 4. Eigenvectors and eigenvalues of the first four principal components of 36 bread wheat genotypes evaluated for twelve traits

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
Plant height (cm)	0.193	0.405	-0.044	0.001
Days to heading (days)	0.422	0.019	-0.128	-0.200
Grain filling period (days)	0.095	-0.320	-0.006	0.603
Days to maturity (days)	0.440	-0.135	-0.123	0.104
No. of fertile tillers/plant (no.)	-0.297	0.181	-0.332	0.115
Spike length (cm)	0.257	0.331	0.256	-0.114
No. of spikelets/spike (no.)	0.352	0.121	0.151	0.110
No. of kernels/ spike (no.)	0.152	0.386	0.223	0.206
Thousand-kernel weight (g)	-0.171	-0.051	-0.184	0.480
Grain yield (t ha ⁻¹)	-0.187	0.514	-0.074	0.226
Biomass yield (t ha ⁻¹)	0.256	0.252	-0.472	0.285
Harvest index (%)	-0.378	0.271	0.265	0.003
Eigenvalue	4.32	2.37	1.28	1.20
Variance explained (%)	33.24	18.23	9.86	9.23
Cumulative variance explained (%)	33.24	51.47	61.33	70.56
Difference	1.95	1.09	0.08	0.34

3.3. Genetic Divergence Analysis

3.3.1. Genetic distances among wheat genotypes

The genetic distance of all possible pairs of 36 bread wheat genotypes ranged from 1.15 to 9.20 with the mean, standard deviation and coefficient of variation of 4.47, 1.28 and 28.71%, respectively (Table 5). The mean genetic distance, standard deviation and coefficient of variation among four released varieties were 5.20, 1.67 and 32.06%, respectively (Table 5). G19 (KINGBIRD) was distant and G6 (FENTALLE) the closest to check varieties with mean genetic distances of 4.71 and 6.61, respectively. This indicated that the check varieties had lower genetic distances among them than among considerable number of new entries. Arega *et al.* (2007) conducted research on title to estimate the genetic divergence among indigenous durum wheat (*Triticum durum* Desf.) genotypes of diverse origin and clustered them into homogenous groups and suggested an opportunity for improvement of grain yield through hybridization of genotypes from different clusters and subsequent selection from segregating generations for hybridization programmes.

The mean genetic distance of each bread wheat genotype to other 35 genotypes was calculated to generate information on the most distant and closest genotypes (Table 5). Depending on the mean Euclidean distance, G11 (6.22) followed by G8 (6.15) and the check variety, G19 (KINGBIRD) (5.87) was the most distant to other genotypes while the two check varieties, G6 (FENTALLE) and G13 (GAMBO) had mean genetic distances lower than the overall mean genetic distance of genotypes indicating that the varieties were not distant (were close) to the other genotypes. A total of 11 (34.38%) of the new entries had mean genetic distances greater than the overall mean genetic distance of genotypes. The result suggested the presence of considerable number of distant bread wheat genotypes to others that could be used in crossing program to combine the desirable traits of the genotypes. Initiation sound hybridization program needs the availability of genetically divergent genotypes for quantitative characters that contribute towards yield (Singh, 1983); and therefore, in any breeding program, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981).

Table 5. Range and mean Euclidean distance of thirty-six bread wheat genotypes estimated from twelve quantitative traits as evaluated at Mehani in 2017

Genotype	Minimum	Maximum	Mean	SD	CV (%)
G1	1.80	6.41	3.64	1.16	31.89
G2	2.09	6.37	3.79	1.25	32.99
G3	1.89	7.25	4.05	1.49	36.91
G4	1.87	9.05	4.99	1.60	32.12
G5	1.45	6.84	3.87	1.44	37.09
G6	2.37	6.62	3.96	1.21	30.60
G7	3.06	9.20	5.53	1.35	24.41
G8	3.53	9.20	6.15	1.52	24.75
G9	2.64	6.60	4.20	1.12	26.63
G10	2.43	9.00	5.47	1.66	30.40
G11	3.57	8.10	6.22	1.14	18.35
G12	1.18	6.37	3.45	1.16	33.60
G13	2.05	7.62	4.54	1.45	31.94
G14	1.15	6.39	3.60	1.22	33.89
G15	1.73	7.60	4.09	1.40	34.14
G16	2.71	8.52	4.91	1.45	29.45
G17	2.44	7.44	4.47	1.27	28.46
G18	2.44	7.35	4.50	1.35	30.09
G19	3.14	7.76	5.87	1.28	21.82
G20	2.18	8.39	4.96	1.56	31.53
G21	2.24	6.90	4.38	1.14	26.13
G22	2.10	7.02	4.84	1.10	22.70
G23	2.18	7.20	4.06	1.26	30.88
G24	2.10	7.38	4.65	1.29	27.67
G25	1.47	6.48	3.95	1.42	35.95
G26	1.60	6.48	3.89	1.19	30.53
G27	1.15	6.61	3.77	1.18	31.24
G28	1.45	7.10	4.10	1.58	38.59
G29	2.61	7.39	4.96	1.28	25.84
G30	4.32	6.86	5.41	0.73	13.53
G31	2.24	6.13	4.06	0.99	24.34
G32	2.55	8.07	5.11	1.41	27.52
G33	1.60	7.10	4.03	1.35	33.57
G34	2.06	6.29	3.78	1.06	27.99
G35	1.18	6.01	3.48	1.00	28.77
G36	2.04	6.25	4.26	1.15	26.97
Overall	1.15	9.20	4.47	1.28	28.71

3.3.2. Clustering of Genotypes

The Euclidean distance matrix of 630 pair of wheat genotypes estimated from 12 quantitative traits was used to construct dendrograms based on the Unweighted Pair-group methods with Arithmetic Means (UPGMA). Accordingly, the 36 wheat genotypes were grouped into eight distinct clusters (Figure 1 and Table 6). Cluster VI was the largest, and consisted of eleven genotypes (30.56%) of the total genotypes. Cluster VIII consisted of eight (22.22%) and cluster III consisted of six (16.67%) in which cluster III genotypes included two released varieties (Ogolcho and Kingbird). Cluster VII included two released varieties (Fentalle and Gambo), Cluster IV and II with four and six genotypes, respectively, while Cluster I and V consisted only by one genotype. This indicates that the crossing between superior genetic divergences of above diverse clusters might provide desirable recombinants for developing high yielding bread wheat genotypes. This is because cluster analysis grouped genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters (Jaynes *et al.*, 2003).

Several authors reported the presence of divergence among the bread wheat genotypes indicating grouping in different numbers of distinct clusters. Dergicho *et al.* (2015) classified 68 bread wheat germplasm in to six groups; Ahmad *et al.* (2014), classified 19 genotypes into 3 clusters on the basis of average linkage and Salman *et al.* (2014) classified 65 bread wheat genotypes into 6 clusters. Awale and Sentayehu (2013) grouped 26 bread wheat genotypes into six clusters. Likewise, Shashikala (2006) grouped 169 wheat genotypes in to 11 clusters. Ajmal *et al.* (2013) classified 50 genotypes of wheat into 5 clusters while Desheva and Cholakov (2014), categorized winter wheat genotypes into three clusters.

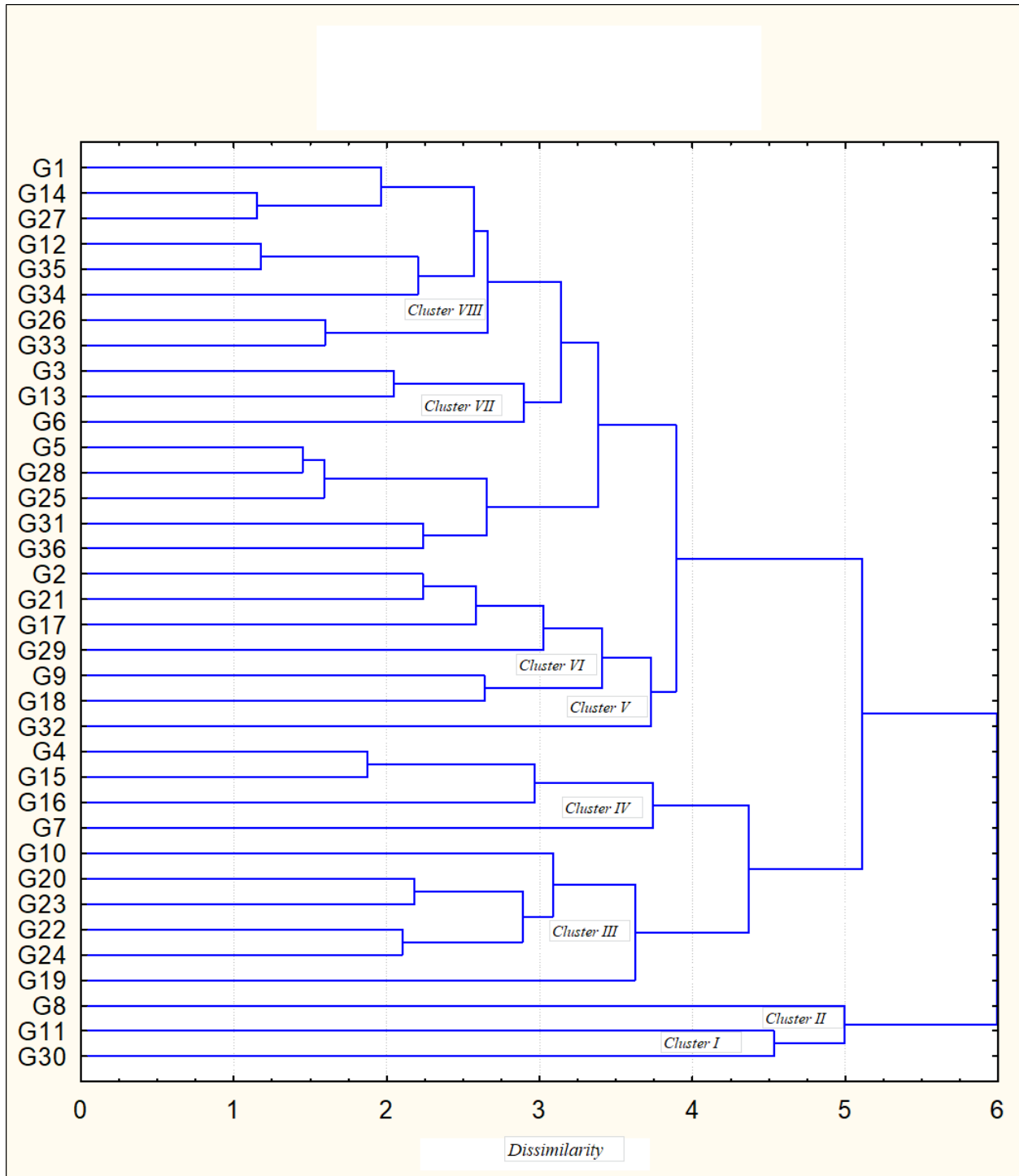


Figure 1. Dendrogram depicting dissimilarity of 36 bread wheat genotypes (G1- G36 genotypes code as description given in Table 1) by Unweighted Pair group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 12 phenological/ growth traits, grain yield and yield components.

Table 6. Distribution of twelve wheat genotypes in to eight different clusters based on twelve quantitative traits evaluated at Mehoni in 2017

Cluster	Number of Genotypes	Genotype (G*)
Cluster I	1 (2.78%)	G30
Cluster II	2 (5.56%)	G8, G11
Cluster III	6 (16.67%)	G10, G19(King bird), G20(Ogolcho), G22, G23, G24
Cluster IV	4 (11.11%)	G4, G7, G15, G16
Cluster V	1 (2.78%)	G32,
Cluster VI	11 (30.56%)	G2, G5, G9, G17, G18, G21, G25, G28, G29, G31, G36
Cluster VII	3 (8.33%)	G3, G6(Fentalle), G13(Gambo)
Cluster VIII	8 (22.22%)	G1, G12, G14, G26, G27, G33, G34, G35

G* Genotypes are numbered as shown on Table 1.

3.3.3. Cluster Mean Analysis

The mean values of eight clusters for 12 quantitative characters are presented in (Table 7). Cluster I and II had mean values greater than overall mean values of genotypes for days to heading, grain filling period, days to maturity, number of spikelets per spike and number of kernels per spike. In addition, Cluster I and II for thousand kernels weight and biomass yield respectively, had mean values greater than overall mean values, but for the remaining traits both clusters had mean values lower than overall mean values of genotypes. Cluster III and IV had mean values greater than overall mean values of genotypes for number of fertile tillers per plant, thousand kernel weight and harvest index. However, Cluster III and IV distinguished each other by having mean values of grain filling period and grain yield greater than overall mean values respectively. These clusters had mean values lower than overall mean values of genotypes for the remaining traits. Adhiena (2015) evaluated 26 bread wheat genotypes at Korem in Southern part of Tigray Regional State which is a few kilometers distance from the current study site but at higher elevation (2490m.a.s.l.). He reported that six genotypes were grouped together in Cluster III that had higher mean grain yield and early maturing habit and suggested that selection for early maturity could be done more effectively from this cluster which could be used for environments with shorter duration of rainfall distribution. The grouping of bread wheat

genotypes in one or two clusters that had desirable traits to be used for crossing and/or selection programs has been reported by other authors.

Cluster VII and VIII had mean values greater than overall mean values of genotypes for number of fertile tillers per plant, number of spikelets per spike, number of kernels per spike, grain yield, biomass yield and harvest index. In addition, Cluster VII had mean values greater than overall mean values of genotypes for plant height and spike length while Cluster VIII had mean values greater than overall mean values for thousand kernel weight. However, these clusters had mean values lower than overall mean values of genotypes for the remaining traits. These two clusters consisted of 11 (30.5%) genotypes with higher grain yield and mean values greater than overall mean values of genotypes for most desirable traits suggesting that selection of genotypes and/or further evaluation of members of these clusters is possible to develop varieties for the study area.

The two clusters (I and II) consisted of three genotypes with low mean grain yield but the members of these clusters were late maturing when compared to the average crop maturity of the genotypes. Cluster III consisted of six genotypes having late grain filling period but with higher mean values for number of fertile tillers per plant, thousand kernel weight and harvest index. Similarly, Cluster V and VI consisted of twelve genotypes characterized as late maturing, tall plants, higher mean values for most spike characters and biological yield, but these clusters had lower mean values for number of fertile tillers per plant, grain yield, thousand kernel weight and harvest index. The genotypes included in these clusters might not be considered for selection and/or further evaluation to develop varieties in the study area due to the undesirable traits of low yield and late maturity since the study area is known by short duration of rainfall period. However, crossing among the members of these clusters and Cluster IV, VII and VIII which consisted of early maturing but high yielding genotypes, might be possible to obtain high yielding and late maturing genotypes from segregating progenies that might be appropriate for areas with long duration of rainfall period.

Cluster IV consisted of four genotypes with the highest mean grain yield among the clusters with early maturing which suggested the advantage of further evaluation of the genotypes in this cluster along with the members of Cluster VII and VIII to develop/identify high yielding variety (ies) for the study area. However, it is also possible to suggest crossing among the genotypes in

Cluster IV and VII to obtain progenies that combine early maturing, highest yield, higher mean values for spike characters, tall plants and high biological yield. But, for obtaining progenies with short plant height and short spike length but with high mean values for other desirable traits (early maturing, high yield, spike characters etc.), it is suggested crossing among genotypes in Cluster IV and VIII. Mean value analysis for clusters revealed the higher chance of obtaining bread wheat genotypes that combine high yield and early maturity (Cluster IV, VII and VIII) that fit the study area having shorter duration of rainfall distribution. It is also possible to use the genotypes as source of genes for early maturity, high yield and for many yield related traits in crossing programs. Salman *et al.* (2014) identified one cluster among six to be used as source of early maturing materials while Desheva and Cholakov (2014) reported genotypes suitable for hybridization programs aimed at developing high yielding wheat varieties.

Table 7. Mean values of characters for eight clusters based on twelve quantitative traits evaluated at Mehoni in 2017

Trait	Cluster								Overall Mean
	I	II	III	IV	V	VI	VII	VIII	
PH (cm)	62.13	81.18	78.38	84.98	89.07	88.52	95.51	85.01	85.7
HD (days)	75	80.89	60.05	66.75	78.33	77.24	71.66	71.04	71.7
GFP (days)	31.33	33.16	31.78	24.92	33.00	28.61	26.47	28.29	28.93
MD (days)	106.33	114.17	91.83	91.67	111.33	105.88	98.11	99.21	100.5
FTPP (no.)	1.97	1.48	2.38	2.67	1.43	1.96	2.25	2.38	2.18
SL (cm)	9.08	8.97	8.39	9.01	11.38	9.90	10.02	9.40	9.46
SPS (no.)	19.7	19.86	16.84	15.94	19.1	19.03	19.02	19.05	18.38
KPS (no.)	48.2	49.25	42.18	40.24	43.93	48.66	50.50	47.09	46.1
TKW (g)	40.4	35.38	38.17	40.73	31.4	33.18	33.20	36.21	35.79
GY (t ha ⁻¹)	3.33	2.92	4.07	4.81	4.11	3.9	4.53	4.63	4.18
BY (t ha ⁻¹)	2.97	3.27	2.65	3.02	3.4	3.14	3.15	3.1	3.05
HI (%)	28.08	22.62	38.69	39.70	30.24	31.38	35.98	37.4	34.61

PH=Plant height (cm), DH=Days to heading, GFP=Grain filling period (days), DM=Days to maturity, FTTP=No. of fertile tillers/plant, SL=Spike length (cm), SPS=No. of spikelets/spike, KPS=No. of kernels/ spike, TKW=Thousand-kernel weight (g), GY=Grain yield (t/ha), BY=Biomass yield (t/ha), HI=Harvest index (%) no.=number.

4. SUMMARY AND CONCLUSIONS

Thirty-six bread wheat genotypes were grown in 2017 at Mehoni Agricultural Research Station in Southern Tigray using 6x6 Triple-Lattice Design to determine genetically divergent bread wheat genotypes with desirable traits for hybridization particularly for yield. To generate such information, data were collected on 12 traits of which some were taken on plot basis while the others were assessed on single plant basis. The four central rows were used for data collection on plot basis.

The analysis of variance revealed highly significant differences among the genotypes for all characters. Principal component analysis showed that the first four principal components having eigen values greater than one accounted for 70.56% of the total variation of the 36 genotypes evaluate for 12 traits. The genetic distances among 36 bread wheat genotypes estimated using Euclidean distance ranged from 1.15 to 9.20 with the mean, standard deviation and coefficient of variation of 4.47, 1.28 and 28.71%, respectively. A total of 11 (34.38%) out of 32 new entries had mean genetic distances greater than the overall mean genetic distance of genotypes. Higher genetic distances were estimated among the new entries than among the four check varieties and check varieties with new entries. The genotypes were grouped into eight distinct clusters of which Cluster VI , VIII and III consisted of 11 (30.56%), 8 (22.22%) and 6 (16.67%) genotypes, respectively. Cluster VII and III were consists of two released varieties (Fentalle and Gambo) and (Ogolcho and Kingbird), Cluster IV, II and V with 3, 4 and 2 genotypes, respectively, while Cluster I was solitary. Cluster IV was distinguished by having the highest mean values for thousand kernel weight (41 g), fertile tillers per plant (3), grain yield (4.8 t ha⁻¹) and harvest index (40) and Cluster V characterized as consisting of genotypes with the highest mean values for spike length and biomass yield. The result suggested the presence of considerable number of distant bread wheat genotypes that could be used in crossing program to combine the desirable traits of the genotypes. However, since this is a one-year result, it is necessary to repeat the field experiment and evaluate the genotypes over several locations and years in order to make conclusive and comprehensive conclusions and recommendations.

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